



SEQUENCE LISTING

<110> Merck & Co., Inc.

LaMonica, Nicola

Facciabene, Andrea

Aurismicchio, Luigi

<120> CARCINOEMBRYONIC ANTIGEN FUSIONS AND
USES THEREOF

<130> ITR0073YP

<140> 10/589,180

<141> 2006-08-11

<150> PCT/EP2005/001114

<151> 2005-02-03

<150> 60/635,791

<151> 2004-12-14

<150> 60/543,649

<151> 2004-02-11

<160> 54

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 1
tattctagat gctccccaga ctattacaga a 31

<210> 2
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer, chemically synthesized

<400> 2
tatgcggccg cctagttttc catactgatt gccgc 35

<210> 3
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer, chemically synthesized

<400> 3
gctctagagc cccccagagc atcaccgagc tgtgc 35

<210> 4
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer, chemically synthesized

<400> 4
gctctagaac ccctcagaac atcaccgatc tgtgcgcc 38

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 5

tattctagat aatggcgaca aattataccg

30

<210> 6

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 6

tatgcggccg ctcataattc atcccgaatt ctggt

35

<210> 7

<211> 2766

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LTA fusion

<400> 7

atggagtctc cctcgcccc tccccacaga tgggtgatcc cctggcagag gtcctgctc 60
acagcctcac ttctaacctt ctggaaccg cccaccactg ccaagctcac tattgaatcc 120
acgccgttca atgtcgaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata 300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360

```

accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
tacccgagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccgt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660
gtgagtgccg ggcgagctga ttcagtcac ctgaatgtcc tctatggccc ggatgcccc 720
accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctctgccac 780
gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgccaa 900
gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
gagccacca aaccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtgggtg ggtaaataat 1080
cagagcctcc cggtcagtcc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140
ctcagtgtca caaggaatga tgtaggaccc tatgagtgtg gaatccagaa cgaattaagt 1200
gttgaccaca gcgacccagt catcctgaat gtcctctatg gccagacga cccaccatt 1260
tccccctcat acacctatta ccgtccagggt gtgaacctca gcctctcctg ccatgcagcc 1320
tctaaccac ctgcacagta ttcttggtg attgatggga acatccagca acacacaaa 1380
gagctcttta tctccaacat cactgagaag aacagcggac tctataacctg ccaggccaat 1440
aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgcggagctg 1500
cccaagccct ccatctccag caacaactcc aaaccctgtg aggacaagga tgctgtggcc 1560
ttcacctgtg aacctgaggg tcagaacaca acctacctgt ggtgggtaaa tggtcagagc 1620
ctcccagtca gtcccagggt gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680
gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gagtgcaaac 1740
cgcagtgaac cagtcacctt ggatgtctc tatgggcccg acacccccat catttcccc 1800
ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggctctaac 1860
ccatccccgc agtattcttg gcgtatcaat gggataccgc agcaacacac acaagttctc 1920
tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980
gctactggcc gcaataattc catagtcaag agcatcacag tctctgcatc tggaactcta 2040
gttaatggcg acaaattata ccgtgctgac tctagacccc cagatgaaat aaaacgttcc 2100
ggaggtctta tgcccagagg gcataatgag tacttcgata gaggaactca aatgaatatt 2160
aatctttatg atcacgcgag aggaacacaa accggctttg tcagatatga tgacggatat 2220
gtttccactt ctcttagttt gagaagtgt cacttagcag gacagtctat attatcagga 2280
tattccactt actatatata tgttatagcg acagcaccaa atatgtttaa tgtaatat 2340
gtattaggcg tatacagccc tcacccatat gaacaggagg tttctgcgtt aggtggaata 2400
ccatattctc agatatatgg atggtatcgt gttaattttg gtgtaattga tgaacgatta 2460
catcgtaaca gggaaatatag agaccggtat tacagaaatc tgaatatagc tccggcagag 2520
gatggttaca gattagcagg tttcccaccg gatcaccaag cttggagaga agaaccctgg 2580

```

attcatcatg caccacaagg ttgtggaaat tcatcaagaa caattacaga tgatacttgt 2640
aatgaggaga cccagaatct gagcacaata tatctcagga aatatcaatc aaaagttaag 2700
aggcagatat tttcagacta tcagtcagag gttgacatat ataacagaat tcgggatgaa 2760
ttatga 2766

<210> 8

<211> 921

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 8

Met	Glu	Ser	Pro	Ser	Ala	Pro	Pro	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
1				5					10					15	
Arg	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
			20					25					30		
Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
		35					40				45				
Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
	50					55				60					
Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
65				70					75					80	
Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser
			85					90					95		
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile
		100					105						110		
Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp
		115					120					125			
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
	130					135					140				
Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys
145				150					155					160	
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr
			165					170					175		
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln

180	185	190
Leu Ser Asn Gly Asn Arg Thr	Leu Thr Leu Phe Asn Val Thr Arg Asn	
195	200	205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg		
210	215	220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn		
245	250	255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser		
290	295	300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala		
305	310	315
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu		
325	330	335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr		
340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg		
355	360	365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr		
370	375	380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser		
385	390	395
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp		
405	410	415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn		
420	425	430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser		
435	440	445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile		
450	455	460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn		
465	470	475
		480

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val			
	485	490	495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro			
	500	505	510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln			
	515	520	525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser			
	530	535	540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn			
	545	550	555
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser			
	565	570	575
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly			
	580	585	590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly			
	595	600	605
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln			
	610	615	620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu			
	625	630	635
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe			
	645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile			
	660	665	670
Thr Val Ser Ala Ser Gly Thr Leu Val Asn Gly Asp Lys Leu Tyr Arg			
	675	680	685
Ala Asp Ser Arg Pro Pro Asp Glu Ile Lys Arg Ser Gly Gly Leu Met			
	690	695	700
Pro Arg Gly His Asn Glu Tyr Phe Asp Arg Gly Thr Gln Met Asn Ile			
	705	710	715
Asn Leu Tyr Asp His Ala Arg Gly Thr Gln Thr Gly Phe Val Arg Tyr			
	725	730	735
Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser Leu Arg Ser Ala His Leu			
	740	745	750
Ala Gly Gln Ser Ile Leu Ser Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val			
	755	760	765
Ile Ala Thr Ala Pro Asn Met Phe Asn Val Asn Asp Val Leu Gly Val			

770	775	780
Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu Gly Gly Ile		
785	790	795
Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe Gly Val Ile		800
	805	810
Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg		815
	820	825
Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu Ala Gly Phe		830
	835	840
Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile His His Ala		845
	850	855
Pro Gln Gly Cys Gly Asn Ser Ser Arg Thr Ile Thr Asp Asp Thr Cys		860
865	870	875
Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg Lys Tyr Gln		880
	885	890
Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser Glu Val Asp		895
	900	905
Ile Tyr Asn Arg Ile Arg Asp Glu Leu		910
	915	920

<210> 9

<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 9

```

atggagtctc cctcggtccc tccccacaga tgggtgcatcc cctggcagag gctcctgctc 60
acagcctcac ttctaacctt ctggaaccgc cccaccactg ccaagctcac tattgaatcc 120
acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata 300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420

```



```

taccgggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccgtg cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660
gtgagtgccg ggcgcagtga ttcagtcctc ctgaatgtcc tctatggccc ggatgcccc 720
accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctctgccac 780
gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgccaa 900
gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
gagccacca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtgggtg ggtaaataat 1080
cagagcctcc cggtcagtcc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140
ctcagtgtca caaggaatga tgtaggaccc tatgagtgtg gaatccagaa cgaattaagt 1200
gttgaccaca ggcacccagt catcctgaat gtcctctatg gccagacga cccaccatt 1260
tccccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg ccatgcagcc 1320
tctaaccac ctgcacagta ttcttggtg attgatggga acatccagca acacacaaa 1380
gagctcttta tctccaatc cactgagaag aacagcggac tctatacctg ccaggccaat 1440
aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgcgagctg 1500
cccaagccct ccatctccag caacaactcc aaaccctgtg aggacaagga tgctgtggcc 1560
ttcacctgtg aacctgaggc tcagaacaca acctacctgt ggtgggtaaa tggtcagagc 1620
ctcccagtca gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680
gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gagtgcacaa 1740
cgcagtgacc cagtcacctt ggatgtctc tatgggcccg acaccccat catttcccc 1800
ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggctctaac 1860
ccatccccgc agtattcttg gcgtatcaat gggataccgc agcaacacac acaagttctc 1920
tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980
gctactggcc gcaataatc catagtcaag agcatcacag tctctgcac tggaactcta 2040
gatgctcccc agtctattac agaactatgt tcggaatatc gcaacacaca aatatatacg 2100
ataaatgaca agatactatc atatacgga tcgatggcag gtaaaagaga aatgggttatc 2160
attacattta agagcggcgc aacatttcag gtcgaagtcc cgggcagtca acatatagac 2220
tccccaaaaa aagccattga aaggatgaag gacacattaa gaatcacata tctgaccgag 2280
accaaatttg ataaattatg tgtatggaat aataaaacc ccaattcaat tgcggaatc 2340
agtatggaaa actag 2355

```

<210> 10

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 10

```

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
 1           5           10           15
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20           25           30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      35           40           45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
      50           55           60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65           70           75           80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
      85           90           95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
      100          105          110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
      115          120          125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130          135          140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145          150          155          160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
      165          170          175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
      180          185          190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
      195          200          205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
      210          215          220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225          230          235          240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn

```

- 11 -

Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn			
545	550	555	560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser			
	565	570	575
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly			
	580	585	590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly			
	595	600	605
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln			
	610	615	620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu			
625	630	635	640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe			
	645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile			
	660	665	670
Thr Val Ser Ala Ser Gly Thr Leu Asp Ala Pro Gln Ser Ile Thr Glu			
	675	680	685
Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys			
	690	695	700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile			
705	710	715	720
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser			
	725	730	735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr			
	740	745	750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val			
	755	760	765
Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn			
	770	775	780

<210> 11

<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAopt-LTB fusion

<400> 11

```

atggagagcc ccagcgcccc cccccaccgc tgggtgcatcc cctggcagcg cctgctgctg 60
accgccagcc tgctgacctt ctggaacccc cccaccaccg ccaagctgac catcgagagc 120
accccccttca acgtggccga gggcaaggag gtgctgctgc tgggtgcaca cctgccccag 180
cacctgttcg gctacagctg gtacaagggc gagcgctgg acggcaaccg ccagatcatc 240
ggctacgtga tcggcaccca gcaggccacc cccggccccg cctacagcgg ccgcgagatc 300
atctaccca acgccagcct gctgatccag aacatcatcc agaacgacac cggcttctac 360
accctgcacg tgatcaagag cgacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccgccagc tgcccaagcc cagcatcagc agcaacaaca gcaagcccg ggaggacaag 480
gacgccgtgg ccttcacctg cgagcccag acccaggacg ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccg gagccccgc ctgcagctga gcaacggcaa ccgcaccctg 600
accctgttca acgtgacctg caacgacacc gccagctaca agtgcgagac ccagaacccc 660
gtgagcgccc gccgcagcga cagcgtgatc ctgaacgtgc tgtacggccc cgacgcccc 720
accatcagcc ccctgaacac cagctaccgc agcggcgaga acctgaacct gagctgccac 780
gccgccagca accccccgc ccagtacagc tggttcgtga acggcacctt ccagcagagc 840
accaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta cacctgccag 900
gccacaaca gcgacaccgg cctgaaccgc accaccgtga ccaccatcac cgtgtacgcc 960
gagcccccca agcccttcat caccagcaac aacagcaacc ccgtggagga cgaggacgcc 1020
gtggccctga cctgcgagcc cgagatccag aacaccacct acctgtggtg ggtgaacaac 1080
cagagcctgc ccgtgagccc ccgcctgcag ctgagcaacg acaaccgcac cctgacctg 1140
ctgagcgtga cccgcaacga cgtgggcccc tacgagtgcg gcatccagaa cgagctgagc 1200
gtggaccaca gcgaccccg gatcctgaac gtgctgtacg gccccgacga cccaccatc 1260
agccccagct acacctacta ccgccccggc gtgaacctga gcctgagctg ccacgcggcc 1320
agcaaccccc ccgcccagta cagctggctg atcgacggca acatccagca gcacaccag 1380
gagctgttca tcagcaacat caccgagaag aacagcggcc tgtacacctg ccaggccaac 1440
aacagcgcca gcggccacag ccgcaccacc gtgaagacca tcaccgtgag cgccgagctg 1500
cccaagcca gcatcagcag caacaacagc aagcccgtgg aggacaagga cgccgtggcc 1560
ttcacctgcg agcccaggc ccagaacacc acctacctgt ggtgggtgaa cggccagagc 1620
ctgcccgtga gccccgcct gcagctgagc aacggcaacc gcacctgac cctgttcaac 1680
gtgaccgcga acgacgcccg cgcctacgtg tgccgcatcc agaacagcgt gagcgccaac 1740
cgcagcgacc ccgtgacctt ggacgtgctg tacggccccg acacccccat catcagcccc 1800
cccgacagca gctacctgag cggcgccaac ctgaacctga gctgccacag cgccagcaac 1860
cccagcccc agtacagctg gcgcatcaac ggcatcccc agcagcacac ccaggtgctg 1920
ttcatcgcca agatcacccc caacaacaac ggcacctacg cctgcttcgt gagcaacctg 1980

```

```

gccaccggcc gcaacaacag catcgtgaag agcatcaccg tgagcgccag cggcacctct 2040
agagctcccc agactattac agaactatgt tcggaatata gcaacacaca aatatatacg 2100
ataaatgaca agatactatc atatacggaa tcgatggcag gcaaaagaga aatgggttatc 2160
attacattta agagcggcga aacatttcag gtcgaagtcc cgggcagtca acatatagac 2220
tcccagaaaa aagccattga aaggatgaag gacacattaa gaatcacata tctgaccgag 2280
accaaattg ataaattatg tgtatggaat aataaaaccc ccaattcaat tgcggcaatc 2340
agtatggaaa actag 2355

```

<210> 12

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAopt-LTBopt fusion

<400> 12

```

atggagagcc ccagcgcccc cccccaccgc tgggtgcatcc cctggcagcg cctgctgctg 60
accgccagcc tgctgacctt ctggaacccc cccaccaccg ccaagctgac catcgagagc 120
acccccctca acgtggccga gggcaaggag gtgctgctgc tgggtgcacaa cctgccccag 180
cacctgttcg gctacagctg gtacaagggc gagcgcgctg acggcaaccg ccagatcatc 240
ggctacgtga tcggcaccca gcaggccacc cccggccccg cctacagcgg ccgcgagatc 300
atctaccca acgccagcct gctgatccag aacatcatcc agaacgacac cggtctctac 360
accctgcacg tgatcaagag cgacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccgccagc tgcccaagcc cagcatcagc agcaacaaca gcaagcccggt ggaggacaag 480
gacgccgtgg ccttcacctg cgagcccagc acccaggacg ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccgt gagccccgc ctgcagctga gcaacggcaa ccgcaccctg 600
accctgttca acgtgacccg caacgacacc gccagctaca agtgcgagac ccagaacccc 660
gtgagcgccc gccgcagcga cagcgtgatc ctgaacgtgc tgtacggccc cgacgcccc 720
accatcagcc ccctgaacac cagctaccgc agcggcgaga acctgaacct gagctgccac 780
gccgccagca accccccgc ccagtacagc tggttcgtga acggcacctt ccagcagagc 840
accaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta cacctgccag 900
gccacaaca gcgacaccgg cctgaaccgc accaccgtga ccaccatcac cgtgtacgcc 960
gagccccca agcccttcat caccagcaac aacagcaacc ccgtggagga cgaggacgcc 1020
gtggccctga cctgcgagcc cgagatccag aacaccacct acctgtggtg ggtgaacaac 1080
cagagcctgc ccgtgagccc ccgcctgcag ctgagcaacg acaaccgcac cctgaccctg 1140
ctgagcgtga cccgcaacga cgtgggcccc tacgagtgcg gcatccagaa cgagctgagc 1200

```

```

gtggaccaca ggcaccccggt gatcctgaac gtgctgtacg gccccgacga cccaccatc 1260
agccccagct acacctacta ccgccccggc gtgaacctga gcctgagctg ccacgccgcc 1320
agcaaccccc ccgcccagta cagctggctg atcgacggca acatccagca gcacaccag 1380
gagctgttca tcagcaacat caccgagaag aacagcggcc tgtacacctg ccaggccaac 1440
aacagcgcca gcggccacag ccgcaccacc gtgaagacca tcaccgtgag cgccgagctg 1500
cccaagccca gcatcagcag caacaacagc aagcccgtgg aggacaagga cgccgtggcc 1560
ttcacctgcg agcccgaggc ccagaacacc acctacctgt ggtgggtgaa cggccagagc 1620
ctgcccgtga gccccgcct gcagctgagc aacggcaacc gcaccctgac cctgttcaac 1680
gtgaccgcga acgacgcccg cgctacgtg tgcggcatcc agaacagcgt gagcgccaac 1740
cgcagcgacc ccgtgaccct ggacgtgctg tacggccccg acacccccat catcagcccc 1800
cccgacagca gctacctgag cggcgccaac ctgaacctga gctgccacag cgccagcaac 1860
cccagcccc agtacagctg gcgcatcaac ggcaccccc agcagcacac ccagggtgctg 1920
ttcatcgcca agatcacccc caacaacaac ggcacctacg cctgcttcgt gagcaacctg 1980
gccaccggcc gcaacaacag catcgtgaag agcatcaccc tgagcgccag cggcacctct 2040
agagcccccc agagcatcac cgagctgtgc agcgagtacc ggaacaccca gatctacacc 2100
atcaacgaca agatcctgag ctacaccgag agcatggccg gcaagagggga gatggtgatc 2160
atcaccttca agagcggcgc caccttccag gtggaggtgc ccggcagcca gcacatcgac 2220
agccagaaga aggccatcga gcggatgaag gacaccctgc ggatcaccta cctcaccgag 2280
accaagatcg acaagctgtg cgtgtggaac aacaagaccc ccaacagcat cgccgccatc 2340
agcatggaga attgataa                                     2358

```

<210> 13

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEAOpt-LTBopt fusion

<400> 13

```

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
  1             5             10             15
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20             25             30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      35             40             45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly

```

50	55	60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile		
65	70	75
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser		80
	85	90
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile		95
	100	105
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp		110
	115	120
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		125
	130	135
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys		140
	145	150
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr		155
	165	170
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln		175
	180	185
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn		190
	195	200
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg		205
	210	215
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		220
	225	230
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn		235
	245	250
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe		255
	260	265
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		270
	275	280
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser		285
	290	295
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala		300
	305	310
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu		315
	325	330
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr		335
	340	345
		350

- 17 -

645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile		
660	665	670
Thr Val Ser Ala Ser Gly Thr Ser Arg Ala Pro Gln Ser Ile Thr Glu		
675	680	685
Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys		
690	695	700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile		
705	710	715
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser		
725	730	735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr		
740	745	750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val		
755	760	765
Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn		
770	775	780

<210> 14

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEAopt-LTBopt fusion

<400> 14

```

atgggcagcc ccagcgcccc cctgcaccgc tgggtgcatcc cctggcagac cctgctgctg 60
accgccagcc tgctgacctt ctggaacccc cccaccaccg cccagctgac catcgagagc 120
cgcccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
agctgctgta tccgcaccca gcagatcacc cccggccccg cccacagcgg cgcgagacc 300
atcgacttca acgccagcct gctgatccac aacgtgaccc agagcgacac cggcagctac 360
accatccagg tgatcaagga ggacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccgccagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccggt ggaggacaag 480
gacgccgtgg ccctgacctg cgagcccag acccaggaca ccacctacct gtgggtgggtg 540

```

```

aacaaccaga gcctgcccgt gagccccgc ctggagctga gcagcgacaa ccgcaccctg 600
accgtgttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
gtgagcgtgc gccgcagcga ccccgtagacc ctgaacgtgc tgtacggccc cgacgcccc 720
accatcagcc ccctgaacac cccctaccgc gccggcgaga acctgaacct gacctgccac 780
gccgccagca accccaccgc ccagtacttc tggttcgtga acggcacctt ccagcagagc 840
acccaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta catgtgccag 900
gccacaaca gcgccaccgg cctgaaccgc accaccgtga ccgccatcac cgtgtacgcc 960
gagctgccc aagccctacat caccagcaac aacagcaacc ccatcgagga caaggacgcc 1020
gtgaccctga cctgcgagcc cgagaccag gacaccacct acctgtggtg ggtgaacaac 1080
cagagcctga gcgtgagcag ccgcctggag ctgagcaacg acaaccgcac cctgaccgtg 1140
ttcaacatcc cccgcaacga caccaccttc tacgagtgcg agaccagaa ccccgtagac 1200
gtgcgccga gcgacccgt gaccctgaac gtgctgtacg gccccgacgc cccaccatc 1260
agccccctga acacccccta ccgcgccggc gagaacctga acctgagctg ccacgccgc 1320
agcaaccccg ccgccagta cagctggttc gtgaacggca ccttcagca gagcaccag 1380
gagctgttca tccccaatc caccgtgaac aacagcggca gctacatgtg ccaggccac 1440
aacagcgcca ccggcctgaa ccgcaccacc gtgaccgcca tcaccgtgta cgtggagctg 1500
cccaagccct acatcagcag caacaacagc aaccccatcg aggacaagga cgccgtgacc 1560
ctgacctgcg agcccgtggc cgagaacacc acctacctgt ggtgggtgaa caaccagagc 1620
ctgagcgtga gccccgcct gcagctgagc aacggcaacc gcatcctgac cctgctgagc 1680
gtgaccgca acgacaccgg cccctacgag tgcggcatcc agaacagcga gagcgccaag 1740
cgcagcgacc ccgtgacct gaacgtgacc tacggccccg acaccccat catcagcccc 1800
cccgacctga gctaccgcag ccgcgccaac ctgaacctga gctgccacag cgacagcaac 1860
cccagcccc agtacagctg gctgatcaac ggcaccctgc gccagcacac ccaggtgctg 1920
ttcatcagca agatcaccag caacaacagc ggcgcctacg cctgcttcgt gagcaacctg 1980
gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040
agagcccccc agagcatcac cgagctgtgc agcaggtacc ggaacaccca gatctacacc 2100
atcaacgaca agatcctgag ctacaccgag agcatggccg gcaagaggga gatggtgatc 2160
atcaccttca agagcggcgc caccttcag gtggaggtgc ccggcagcca gcacatcgac 2220
agccagaaga aggccatcga gcggatgaag gacaccctgc ggatcaccta cctcaccgag 2280
accaagatcg acaagctgtg cgtgtggaac aacaagacc ccaacagcat cgccgccatc 2340
agcatggaga attgataa

```

2358

<210> 15

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEAopt-LTBopt fusion

<400> 15

```

Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
 1           5           10           15
Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20           25           30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
      35           40           45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
      50           55           60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65           70           75           80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
      85           90           95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
      100          105          110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
      115          120          125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130          135          140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145          150          155          160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
      165          170          175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
      180          185          190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
      195          200          205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
      210          215          220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225          230          235          240
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
      245          250          255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe

```

260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser		
290	295	300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala		
305	310	315
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu		
325	330	335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr		
340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg		
355	360	365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro		
370	375	380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser		
385	390	395
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp		
405	410	415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn		
420	425	430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser		
435	440	445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile		
450	455	460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His		
465	470	475
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val		
485	490	495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro		
500	505	510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu		
515	520	525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser		
530	535	540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser		
545	550	555
		560

Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser		
	565	570 575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly		
	580	585 590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly		
	595	600 605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln		
	610	615 620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu		
	625	630 635 640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe		
	645	650 655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile		
	660	665 670
Ser Val Ser Ser Gly Asp Ser Ser Arg Ala Pro Gln Ser Ile Thr Glu		
	675	680 685
Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys		
	690	695 700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile		
	705	710 715 720
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser		
	725	730 735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr		
	740	745 750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val		
	755	760 765
Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn		
	770	775 780

<210> 16

<211> 2118

<212> DNA

<213> Macaca mulatta

<400> 16

atgggggtctc cctcagcccc tcttcacaga tgggtgcatcc cctggcagac gctcctgctc 60

```

acagcctcac tttaaacctt ctggaacccg cccaccactg cccagctcac tattgaatcc 120
aggccgttca atgttgacaga ggggaaggag gttcttctac ttgcccacaa tgtgtcccag 180
aatctttttg gctacatttg gtacaaggga gaaagagtgg atgccagccg tcgaattgga 240
tcatgtgtaa taagaactca acaaattacc ccagggcccg cacacagcgg tcgagagaca 300
atagacttca atgcatccct gctgatccac aatgtcaccc agagtgcacac aggatcctac 360
accatacaag tcataaagga agatcttgtg aatgaagaag caactggcca gttccgggta 420
taccgggagc tgcccaagcc ctacatctcc agcaacaact ccaaccccggt ggaggacaag 480
gatgctgtgg ccttaacctg tgaacctgag actcaggaca caacctacct gtgggtgggta 540
aacaatcaga gcctcccggg cagtcccagg ctggagctgt ccagtgcaca caggaccctc 600
actgtattca atattccaag aaatgcacac acatcctaca aatgtgaaac ccagaaccca 660
gtgagtgatc gacgcagcga cccagtcacc ctgaacgtcc tctatggccc ggatgcgccc 720
accatttccc ctctaaacac accttacaga gcaggggaaa atctgaacct cacctgccac 780
gcagcctcta acccaactgc acagtacttt tggtttgtca atgggacgtt ccagcaatcc 840
acacaagagc tctttatacc caacatcacc gtgaataata gcggatccta tatgtgcca 900
gcccataact cagccactgg cctcaatagg accacagtca cggcgatcac agtctacgcg 960
gagctgcca agccctacat caccagcaac aactccaacc ccatagagga caaggatgct 1020
gtgaccttaa cctgtgaacc tgagactcag gacacaacct acctgtggtg ggtaaacaat 1080
cagagcctct cggtcagttc caggctggag ctgtccaatg acaacaggac cctcactgta 1140
ttcaatattc caagaaacga cacaacgttc tacgaatgtg agaccagaa cccagtgagt 1200
gtcagacgca gcgaccagc caccctgaat gtcctctatg gcccgatgc gccaccatt 1260
tcccctctaa acacacctta cagagcaggg gaaaatctga acctctcctg ccacgcagcc 1320
tctaaccag ctgcacagta ctcttggttt gtcaatggga cgttccagca atccacacaa 1380
gagctcttta taccacacat caccgtgaat aatagcggat cctatatgtg ccaagcccat 1440
aactcagcca ctggcctcaa taggaccaca gtcacggcga tcacagtcta tgtggagctg 1500
cccaagccct acatctccag caacaactcc aaccccatag aggacaagga tgctgtgacc 1560
ttaacctgtg aacctgtggc tgagaacaca acctacctgt ggtgggtaaa caatcagagc 1620
ctctcggta gtcccaggct gcagctctcc aatggcaaca ggatcctcac tctactcagt 1680
gtcacacgga atgacacagg accctatgaa tgtggaatcc agaactcaga gagtgcacaa 1740
cgcagtgacc cagtcacct gaatgtcacc tatggcccag acaccccat catatcccc 1800
ccagacttgt cttaccgttc gggagcaaac ctcaacctct cctgccactc ggactctaac 1860
ccatccccgc agtattcttg gcttatcaat gggacactgc ggcaacacac acaagttctc 1920
tttatctcca aaatcacatc aaacaatagc ggggcctatg cctgttttgt ctctaacttg 1980
gctaccggtc gcaataactc catagtcaag aacatctcag tctcctctgg cgattcagca 2040
cctggaagtt ctggctctct agctagggct actgtcggca tcataattgg aatgctgggt 2100
ggggttgctc tgatgtag 2118

```

<211> 2118

<212> DNA

<213> *Macaca mulatta*

<400> 17

```

atgggggtctc cctcagcccc tcttcacaga tgggtgcatcc cctggcagac gctcctgctc 60
acagcctcac ttctaacctt ctggaacccg cccaccactg cccagctcac tattgaatcc 120
aggccgttca atgttgacaga ggggaaggag gttcttctac ttgcccacaa tgtgtcccag 180
aatctttttg gctacatttg gtacaaggga gaaagagtgg atgccagccg tcgaattgga 240
tcatgtgtaa taagaactca acaaattacc ccagggcccg cacacagcgg tcgagagaca 300
atagacttca atgcatccct gctgatccac aatgtcacc agagtgcacac aggatcctac 360
accatacaag tcataaagga agatcttggt aatgaagaag caactggcca gttccgggta 420
taccgggagc tgcccagacc ctacatctcc agcaacaact ccaaccccggt ggaggacaag 480
gatgctgtgg ccttaacctg tgaacctgag actcaggaca caacctacct gtggtgggta 540
aacaatcaga gcctcccggg cagtcccagg ctggagctgt ccagtgcaca caggaccctc 600
actgtattca atattccaag aatgcacaca acatcctaca aatgtgaaac ccagaaccca 660
gtgagtgtca gacgcagcga cccagtcacc ctgaacgtcc tctatggccc ggatgcgccc 720
accatttccc ctctaaacac acctacaga gcaggggaaa atctgaacct cacctgccac 780
gcagcctcta acccaactgc acagtacttt tggtttgtca atgggacgtt ccagcaatcc 840
acacaagagc tctttatacc caacatcacc gtgaataata gcggatccta tatgtgcca 900
gcccataact cagccactgg cctcaatagg accacagtca cggcgatcac agtctacgcg 960
gagctgccc aagccctacat caccagcaac aactccaacc ccatagagga caaggatgct 1020
gtgaccttaa cctgtgaacc tgagactcag gacacaacct acctgtggtg ggtaaacaat 1080
cagagcctct cggtcagttc caggctggag ctgtccaatg acaacaggac cctcactgta 1140
ttcaatattc caagaaacga cacaacgttc tacgaatgtg agaccagaa cccagtgagt 1200
gtcagacgca gcgaccagc caccctgaat gtcctctatg gcccgatgc gccaccatt 1260
tcccctctaa acacacctta cagagcaggg gaaaatctga acctctcctg ccacgcagcc 1320
tctaaccag ctgcacagta cttttgggtt gtcaatggga cgttccagca atccacaaa 1380
gagctcttta taccacacat caccgtgaat aatagcggat cctatatgtg ccaagcccat 1440
aactcagcca ctggcctcaa taggaccaca gtcacggcga tcacagtcta tgtggagctg 1500
cccaagccct acatctccag caacaactcc aaccccatag aggacaagga tgctgtgacc 1560
ttaacctgtg aacctgtggc tgagaacaca acctacctgt ggtgggtaaa caatcagagc 1620
ctctcgggtc gtcccaggct gcagctctcc aatggcaaca ggatcctcac tctactcagt 1680
gtcacacgga atgacacagg accctatgaa tgtggaatcc agaactcaga gagtgcacaaa 1740
cgcagtgacc cagtcacct gaatgtcacc tatggcccag acaccccat catatcccc 1800
ccagacttgt cttaccgttc gggagcaaac ctcaacctct cctgccactc ggactctaac 1860
ccatccccgc agtattcttg gcttatcaat gggacactgc ggcaacacac acaagttctc 1920

```


tttatctcca aaatcacatc aaacaataac ggggcctatg cctgttttgt ctctaacttg 1980
gctaccggtc gcaataactc catagtcaag aacatctcag tctcctctgg cgattcagca 2040
cctggaagtt ctggtctctc agctagggt actgtcggca tcataattgg aatgctgggt 2100
ggggttgctc tgatgtag 2118

<210> 18

<211> 705

<212> PRT

<213> Macaca mulatta

<400> 18

Met	Gly	Ser	Pro	Ser	Ala	Pro	Leu	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
1				5					10					15	
Thr	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
			20					25					30		
Thr	Ala	Gln	Leu	Thr	Ile	Glu	Ser	Arg	Pro	Phe	Asn	Val	Ala	Glu	Gly
		35					40				45				
Lys	Glu	Val	Leu	Leu	Leu	Ala	His	Asn	Val	Ser	Gln	Asn	Leu	Phe	Gly
	50					55				60					
Tyr	Ile	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Ala	Ser	Arg	Arg	Ile	Gly
65				70					75					80	
Ser	Cys	Val	Ile	Arg	Thr	Gln	Gln	Ile	Thr	Pro	Gly	Pro	Ala	His	Ser
			85					90					95		
Gly	Arg	Glu	Thr	Ile	Asp	Phe	Asn	Ala	Ser	Leu	Leu	Ile	His	Asn	Val
		100						105					110		
Thr	Gln	Ser	Asp	Thr	Gly	Ser	Tyr	Thr	Ile	Gln	Val	Ile	Lys	Glu	Asp
		115					120					125			
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
		130				135					140				
Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	Asp	Lys
145				150					155					160	
Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr	Thr	Tyr
			165					170					175		
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Glu
		180						185					190		
Leu	Ser	Ser	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro	Arg	Asn
		195					200					205			

```

Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
  210                      215                      220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
  225                      230                      235                      240
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
                      245                      250                      255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
                      260                      265                      270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
                      275                      280                      285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
                      290                      295                      300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
  305                      310                      315                      320
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
                      325                      330                      335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
                      340                      345                      350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
                      355                      360                      365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
                      370                      375                      380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
  385                      390                      395                      400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
                      405                      410                      415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
                      420                      425                      430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
                      435                      440                      445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
                      450                      455                      460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
  465                      470                      475                      480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
                      485                      490                      495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro

```

500							505						510				
Ile	Glu	Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Val	Ala	Glu		
515							520						525				
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser		
530							535						540				
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Ile	Leu	Thr	Leu	Leu	Ser		
545							550						555				
Val	Thr	Arg	Asn	Asp	Thr	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Ser		
565							570						575				
Glu	Ser	Ala	Lys	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Thr	Tyr	Gly		
580							585						590				
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Leu	Ser	Tyr	Arg	Ser	Gly		
595							600						605				
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Asp	Ser	Asn	Pro	Ser	Pro	Gln		
610							615						620				
Tyr	Ser	Trp	Leu	Ile	Asn	Gly	Thr	Leu	Arg	Gln	His	Thr	Gln	Val	Leu		
625							630						635				
Phe	Ile	Ser	Lys	Ile	Thr	Ser	Asn	Asn	Ser	Gly	Ala	Tyr	Ala	Cys	Phe		
645							650						655				
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Asn	Ile		
660							665						670				
Ser	Val	Ser	Ser	Gly	Asp	Ser	Ala	Pro	Gly	Ser	Ser	Gly	Leu	Ser	Ala		
675							680						685				
Arg	Ala	Thr	Val	Gly	Ile	Ile	Ile	Gly	Met	Leu	Val	Gly	Val	Ala	Leu		
690							695						700				
Met																	
705																	

```
<210> 19
<211> 705
<212> PRT
<213> Macaca mulatta
```

```
<400> 19
Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
  1             5             10             15
```

```

Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20                      25                      30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
      35                      40                      45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
      50                      55                      60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65                      70                      75                      80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
      85                      90                      95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
      100                     105                     110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
      115                     120                     125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130                     135                     140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145                     150                     155                     160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
      165                     170                     175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
      180                     185                     190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
      195                     200                     205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
      210                     215                     220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225                     230                     235                     240
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
      245                     250                     255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
      260                     265                     270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
      275                     280                     285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
      290                     295                     300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala

```

305	310	315	320
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu			
	325	330	335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr			
	340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg			
	355	360	365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro			
	370	375	380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser			
385	390	395	400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp			
	405	410	415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn			
	420	425	430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Phe			
	435	440	445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile			
	450	455	460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His			
465	470	475	480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val			
	485	490	495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro			
	500	505	510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu			
	515	520	525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser			
	530	535	540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser			
545	550	555	560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser			
	565	570	575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly			
	580	585	590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly			
	595	600	605

Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
610 615 620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
625 630 635 640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Asn Gly Ala Tyr Ala Cys Phe
645 650 655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
660 665 670
Ser Val Ser Ser Gly Asp Ser Ala Pro Gly Ser Ser Gly Leu Ser Ala
675 680 685
Arg Ala Thr Val Gly Ile Ile Ile Gly Met Leu Val Gly Val Ala Leu
690 695 700
Met
705

<210> 20
<211> 702
<212> PRT
<213> Homo sapiens

<400> 20
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
35 40 45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp

115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys		
145	150	155
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr		
165	170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln		
180	185	190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn		
195	200	205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg		
210	215	220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn		
245	250	255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser		
290	295	300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala		
305	310	315
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu		
325	330	335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr		
340	345	350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg		
355	360	365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr		
370	375	380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser		
385	390	395
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp		
405	410	415

Asp	Pro	Thr	Ile	Ser	Pro	Ser	Tyr	Thr	Tyr	Tyr	Arg	Pro	Gly	Val	Asn			
					420						425				430			
Leu	Ser	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser			
					435					440					445			
Trp	Leu	Ile	Asp	Gly	Asn	Ile	Gln	Gln	His	Thr	Gln	Glu	Leu	Phe	Ile			
					450					455					460			
Ser	Asn	Ile	Thr	Glu	Lys	Asn	Ser	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Asn			
					465					470					475			480
Asn	Ser	Ala	Ser	Gly	His	Ser	Arg	Thr	Thr	Val	Lys	Thr	Ile	Thr	Val			
					485					490					495			
Ser	Ala	Glu	Leu	Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro			
					500					505					510			
Val	Glu	Asp	Lys	Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Ala	Gln			
					515					520					525			
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Gly	Gln	Ser	Leu	Pro	Val	Ser			
					530					535					540			
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn			
					545					550					555			560
Val	Thr	Arg	Asn	Asp	Ala	Arg	Ala	Tyr	Val	Cys	Gly	Ile	Gln	Asn	Ser			
					565					570					575			
Val	Ser	Ala	Asn	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asp	Val	Leu	Tyr	Gly			
					580					585					590			
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Ser	Ser	Tyr	Leu	Ser	Gly			
					595					600					605			
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Ala	Ser	Asn	Pro	Ser	Pro	Gln			
					610					615					620			
Tyr	Ser	Trp	Arg	Ile	Asn	Gly	Ile	Pro	Gln	Gln	His	Thr	Gln	Val	Leu			
					625					630					635			640
Phe	Ile	Ala	Lys	Ile	Thr	Pro	Asn	Asn	Asn	Gly	Thr	Tyr	Ala	Cys	Phe			
					645					650					655			
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Ser	Ile			
					660					665					670			
Thr	Val	Ser	Ala	Ser	Gly	Thr	Ser	Pro	Gly	Leu	Ser	Ala	Gly	Ala	Thr			
					675					680					685			
Val	Gly	Ile	Met	Ile	Gly	Val	Leu	Val	Gly	Val	Ala	Leu	Ile					
					690					695					700			

<210> 21

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAoptDOMopt fusion

<400> 21

```

atggagagcc ccagcgcccc cccccaccgc tgggtgcatcc cctggcagcg cctgctgctg 60
accgccagcc tgctgacctt ctggaacccc cccaccaccg ccaagctgac catcgagagc 120
accccccttca acgtggccga gggcaaggag gtgctgctgc tgggtgcacaa cctgccccag 180
cacctgttcg gctacagctg gtacaagggc gagcgctgg acggcaaccg ccagatcatc 240
ggctacgtga tcggcaccca gcaggccacc cccggccccg cctacagcgg ccgcgagatc 300
atctaccca acgccagcct gctgatccag aacatcatcc agaacgacac cggcttctac 360
accctgcacg tgatcaagag cgacctggtg aacgaggagg ccaccggcca gttccgctg 420
taccgccagc tgcccaagcc cagcatcagc agcaacaaca gcaagcccggt ggaggacaag 480
gacgccgtgg ccttcacctg cgagcccgag acccaggacg ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccgt gagccccgc ctgcagctga gcaacggcaa ccgcaccctg 600
accctgttca acgtgacccg caacgacacc gccagctaca agtgcgagac ccagaacccc 660
gtgagcgccc gccgcagcga cagcgtgatc ctgaacgtgc tgtacggccc cgacgcccc 720
accatcagcc ccctgaacac cagctaccgc agcggcgaga acctgaacct gagctgccac 780
gccgccagca accccccgc ccagtacagc tggttcgtga acggcacctt ccagcagagc 840
acccaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta cacctgccag 900
gccacaaca gcgacaccgg cctgaaccgc accaccgtga ccaccatcac cgtgtacgcc 960
gagcccccca agcccttcat caccagcaac aacagcaacc ccgtggagga cgaggacgcc 1020
gtggccctga cctgcgagcc cgagatccag aacaccacct acctgtggtg ggtgaacaac 1080
cagagcctgc ccgtgagccc ccgcctgcag ctgagcaacg acaaccgcac cctgaccctg 1140
ctgagcgtga cccgcaacga cgtgggcccc tacgagtgcg gcatccagaa cgagctgagc 1200
gtggaccaca gcgaccccggt gatcctgaac gtgctgtacg gccccgacga cccaccatc 1260
agccccagct acacctacta ccgccccggc gtgaacctga gcctgagctg ccacgccgcc 1320
agcaaccccc ccgcccagta cagctggctg atcgacggca acatccagca gcacaccag 1380
gagctgttca tcagcaacat caccgagaag aacagcggcc tgtacacctg ccaggccaac 1440
aacagcgcca gcggccacag ccgcaccacc gtgaagacca tcacctgag cgccgagctg 1500
cccaagccca gcatcagcag caacaacagc aagcccgctg aggacaagga cgccgtggcc 1560
ttcacctgcg agccccaggc ccagaacacc acctacctgt ggtgggtgaa cggccagagc 1620

```

```

ctgcccgtga gccccgcct gcagctgagc aacggcaacc gcaccctgac cctgttcaac 1680
gtgaccgcga acgacgcccg cgcctacgtg tgcggcatcc agaacagcgt gagcgccaac 1740
cgcagcgacc ccgtgaccct ggacgtgctg tacggccccg acacccccat catcagcccc 1800
cccgacagca gctacctgag cggcgccaac ctgaacctga gctgccacag cgccagcaac 1860
cccagcccc agtacagctg gcgcatcaac ggcatcccc agcagcacac ccagggtgctg 1920
ttcatcgcca agatcacccc caacaacaac ggacacctag cctgcttcgt gagcaacctg 1980
gccaccggcc gcaacaacag catcgtgaag agcatcaccg tgagcgccag cggcacctct 2040
agaagcacc ccatcccatt cagctacagc aagaacctgg actgctgggt ggacaacgag 2100
gaggacatcg acgtgatcct gaagaagagc accatcctga acctggacat caacaacgac 2160
atcatcagcg acatcagcgg cttcaacagc agcgtgatca cctaccccga cgccagctg 2220
gtgcccggca tcaacggcaa ggccatccac ctggtgaaca acgagagcag cgagggtgatc 2280
gtgcacaagg ccatggacat cgagtacaac gacatgttca acaacttcac cgtgagcttc 2340
tggctgagag tgccaaagg gagcgccagc cacctggagc agtacggcac caacgagtac 2400
agcatcatca gcagcatgaa gaagcacagc ctgagcatcg gcagcggctg gagcgtgagc 2460
ctgaagggca acaacctcat ctggaccctg aaggatagcg ccggagaggt gagacagatc 2520
accttcagag acctgcccga caagttcaat gcctacctgg ccaacaagtg ggtgttcac 2580
accatcacca acgacagact gagcagcgcc aacctgtaca tcaacggcgt gctcatgggc 2640
agcgccgaga tcaccggcct gggcgccatc agagaggaca acaacatcac cctgaagctg 2700
gacagatgca acaacaacaa ccagtacgtg agcatcgaca agttccggat cttctgcaag 2760
gccctgaacc ccaaggagat cgagaagctg tacaccagct acctgagcat caccttcctg 2820
agagacttct ggggcaaccc cctgagatac gacacctag 2859

```

<210> 22

<211> 2037

<212> DNA

<213> Artificial Sequence

<220>

<223> deleted human CEA

<400> 22

```

atggagtctc cctcggcccc tccccacaga tgggtgcatcc cctggcagag gctcctgctc 60
acagcctcac ttctaacctt ctggaacctg cccaccactg ccaagctcac tattgaatcc 120
acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggcccc catacagtgg tcgagagata 300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360

```

```

accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
tacccgagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccgt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660
gtgagtgccg ggcgacagtga ttcagtcac ctgaatgtcc tctatggccc ggatgcccc 720
accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctctgccac 780
gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgccaa 900
gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
gagccacca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg ggtaaataat 1080
cagagcctcc cggtcagtcc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140
ctcagtgtca caaggaatga ttaggaccc tatgagtgtg gaatccagaa cgaattaagt 1200
gttgaccaca gcgaccagc catcctgaat gtcctctatg gccagacga cccaccatt 1260
tccccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg ccatgcagcc 1320
tctaaccac ctgcacagta ttcttggctg attgatggga acatccagca acacacaaa 1380
gagctcttta tctccaacat cactgagaag aacagcggac tctataacct ccaggccaat 1440
aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgcggagctg 1500
cccaagccct ccatctccag caacaactcc aaaccctgg aggacaagga tgctgtggcc 1560
ttcacctgtg aacctgaggc tcagaacaca acctacctgt ggtgggtaaa tggtcagagc 1620
ctccagtcg gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680
gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gagtgcaaac 1740
cgcagtgacc cagtcacctt ggatgtctc tatgggccgg acacccccat catttcccc 1800
ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggcctctaac 1860
ccatccccgc agtattcttg gcgtatcaat gggataccgc agcaacacac acaagttctc 1920
tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980
gctactggcc gcaataattc catagtcaag agcatcacag tctctgcac tggaact 2037

```

<210> 23

<211> 679

<212> PRT

<213> Artificial Sequence

<220>

<223> deleted human CEA

<400> 23

```

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
  1              5              10              15
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20              25              30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
      35              40              45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
      50              55              60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
  65              70              75              80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
      85              90              95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
      100              105              110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
      115              120              125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130              135              140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
  145              150              155              160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
      165              170              175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
      180              185              190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
      195              200              205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
      210              215              220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
  225              230              235              240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
      245              250              255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
      260              265              270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
      275              280              285

```

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser			
290	295	300	
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala			
305	310	315	320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu			
325	330	335	
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr			
340	345	350	
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg			
355	360	365	
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr			
370	375	380	
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser			
385	390	395	400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp			
405	410	415	
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn			
420	425	430	
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser			
435	440	445	
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile			
450	455	460	
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn			
465	470	475	480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val			
485	490	495	
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro			
500	505	510	
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln			
515	520	525	
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser			
530	535	540	
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn			
545	550	555	560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser			
565	570	575	
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly			

```

          580              585              590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
          595              600              605
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
          610              615              620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
          625              630              635              640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
          645              650              655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
          660              665              670
Thr Val Ser Ala Ser Gly Thr
          675

```

<210> 24

<211> 3426

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-FRC fusion

<400> 24

```

atggagtctc cctcggtccc tccccacaga tgggtgcatcc cctggcagag gtcctgctc 60
acagcctcac ttctaacctt ctggaacctg cccaccactg ccaagctcac tattgaatcc 120
acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggcccc catacagtgg tcgagagata 300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
taccgaggag tgcccaagcc ctccatctcc agcaacaact ccaaaccctg ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccgtg cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660
gtgagtgccg ggcgcagtga ttcagtcatc ctgaatgtcc tctatggccc ggatgcccc 720
accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctctgcccac 780

```

gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
 acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgccaa 900
 gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
 gagccacca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
 gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg ggtaaataat 1080
 cagagcctcc cggtcagtc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140
 ctcagtgtca caaggaatga ttaggagccc tatgagtgtg gaatccagaa cgaattaagt 1200
 gttgaccaca gcgacccagt catcctgaat gtcctctatg gccagacga cccaccatt 1260
 tccccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg ccatgcagcc 1320
 tctaaccac ctgcacagta ttcttggctg attgatggga acatccagca acacacaaa 1380
 gagctcttta tctccaacat cactgagaag aacagcggac tctataacctg ccaggccaat 1440
 aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgcggagctg 1500
 cccaagccct ccatctccag caacaactcc aaaccctgg aggacaagga tgctgtggcc 1560
 ttcacctgtg aacctgaggc tcagaacaca acctacctgt ggtgggtaaa tggtcagagc 1620
 ctcccagtc gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680
 gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gagtgc aaac 1740
 cgcagtgacc cagtcacct ggatgtcctc tatgggcccg acacccccat catttcccc 1800
 ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggcttctaac 1860
 ccatccccgc agtattcttg gcgtatcaat gggataccgc agcaacacac acaagtctc 1920
 tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980
 gctactggcc gcaataattc catagtcaag agcatcacag tctctgcatc tggaactcta 2040
 gattcaacac caattccatt ttcttattct aaaaatctgg attgttgggt tgataatgaa 2100
 gaagatatag atgttatatt aaaaaagagt acaattttta atttagatat taataatgat 2160
 attatatcag atatatctgg gtttaattca tctgtaataa catatccaga tgctcaattg 2220
 gtgcccggaa taaatggcaa agcaatacat ttagtaacaa atgaatcttc tgaagttata 2280
 gtgcataaag ctatggatat tgaatataat gatatgttta ataattttac cgtagcttt 2340
 tggttgaggg ttcctaaagt atctgctagt catttagaac aatatggcac aaatgagtat 2400
 tcaataatta gctctatgaa aaaacatagt ctatcaatag gatctggttg gagtgtatca 2460
 cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 2520
 acttttaggg atttacctga taaatttaat gcttatttag caaataaatg ggtttttata 2580
 actattacta atgatagatt atcttctgct aatttgtata taaatggagt acttatggga 2640
 agtgcagaaa ttactggttt aggagctatt agagaggata ataataaac attaaaacta 2700
 gatagatgta ataataataa tcaatacgtt tctattgata aatttaggat attttgcaaa 2760
 gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aaccttttta 2820
 agagacttct ggggaaaccc tttacgatat gatacagaat attatttaat accagtagct 2880
 tctagttcta aagatgttca attgaaaaat ataacagatt atatgtattt gacaaatgcg 2940
 ccatcgata ctaacggaaa attgaatata tattatagaa gggttatataa tggactaaaa 3000

```

tttattataa aaagatatac acctaataat gaaatagatt cttttgttaa atcaggtgat 3060
tttattaaat tatatgtatc atataacaat aatgagcaca ttgtaggtta tccgaaagat 3120
ggaaatgcct ttaataatct tgatagaatt ctaagagtag gttataatgc cccaggtatc 3180
cctctttata aaaaaatgga agcagtaaaa ttgctgtgatt taaaaaccta ttctgtacaa 3240
cttaaattat atgatgataa aaatgcatct ttaggactag taggtaccca taatgggtcaa 3300
ataggcaacg atccaaatag ggatatatta attgcaagca actgggtactt taatcattta 3360
aaagataaaa ttttaggatg tgattgggtac tttgtaccta cagatgaagg atggacaaat 3420
gattaa 3426

```

<210> 25

<211> 2664

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-FcIgG fusion

<400> 25

```

atggagagcc ccagcgcccc cccccaccgc tgggtgcatcc cctggcagcg cctgctgctg 60
accgccagcc tgctgacctt ctggaacccc cccaccaccg ccaagctgac catcgagagc 120
acccccttca acgtggccga gggcaaggag gtgctgctgc tgggtgcacaa cctgccccag 180
cacctgttcg gctacagctg gtacaagggc gagcgctggg acggcaaccg ccagatcatc 240
ggctacgtga tcggcaccca gcaggccacc cccggccccg cctacagcgg ccgcgagatc 300
atctacccca acgccagcct gctgatccag aacatcatcc agaacgacac cggcttctac 360
accctgcacg tgatcaagag cgacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccgccagc tgcccaagcc cagcatcagc agcaacaaca gcaagcccggt ggaggacaag 480
gacgccgtgg ccttcacctg cgagcccag acccaggacg ccacctacct gtgggtgggtg 540
aacaaccaga gcctgcccgt gagccccgc ctgcagctga gcaacggcaa ccgcaccctg 600
accctgttca acgtgaccgg caacgacacc gccagctaca agtgcgagac ccagaacccc 660
gtgagcgccc gccgcagcga cagcgtgatc ctgaacgtgc tgtacggccc cgacgcccc 720
accatcagcc ccctgaacac cagctaccgc agcggcgaga acctgaacct gagctgccac 780
gccgccagca accccccgc ccagtacagc tgggttcgtga acggcacctt ccagcagagc 840
accaggagc tgttcacccc caacatcacc gtgaacaaca gcggcagcta cacctgccag 900
gccacaaca gcgacaccgg cctgaaccgc accaccgtga ccaccatcac cgtgtacgcc 960
gagcccccca agcccttcat caccagcaac aacagcaacc ccgtggagga cgaggacgcc 1020
gtggccctga cctgcgagcc cgagatccag aacaccacct acctgtggtg ggtgaacaac 1080
cagagcctgc ccgtgagccc ccgcctgcag ctgagcaacg acaaccgcac cctgaccctg 1140

```



```

ctgagcgtga cccgcaacga cgtgggcccc tacgagtgcg gcatccagaa cgagctgagc 1200
gtggaccaca gcgaccccggt gatcctgaac gtgctgtacg gccccgacga cccaccatc 1260
agccccagct acacctacta ccgccccggc gtgaacctga gcctgagctg ccacgccgcc 1320
agcaaccccc ccgcccagta cagctgggctg atcgacggca acatccagca gcacaccag 1380
gagctgttca tcagcaacat caccgagaag aacagcggcc tgtacacctg ccaggccaac 1440
aacagcgcca gcggccacag ccgcaccacc gtgaagacca tcaccgtgag cgccgagctg 1500
cccaagccca gcatcagcag caacaacagc aagcccgtgg aggacaagga cgccgtggcc 1560
ttcacctgcg agccccagggc ccagaacacc acctacctgt ggtgggtgaa cggccagagc 1620
ctgcccgtga gccccgcct gcagctgagc aacggcaacc gcaccctgac cctgttcaac 1680
cgcagcgacc ccgtgaccct ggacgtgctg tacggccccg acacccccat catcagcccc 1740
cccagacagca gctacctgag cggcgccaac ctgaacctga gctgccacag cgccagcaac 1800
cccagcccc agtacagctg gcgcatcaac ggcaccccc agcagcacac ccaggtgctg 1860
ttcatcgcca agatcacccc caacaacaac ggcacctacg cctgcttcgt gagcaacctg 1920
gccaccggcc gcaacaacag catcgtgaag agcatcaccg tgagcgccag cggcacctct 1980
agaaagaccc acacctgccc cccttgccct gccctgagc tgctgggcgg acccagcgtg 2040
ttcctgttcc cccccaagcc taaggacacc ctcatgatca gcagaacccc cgaggtgacc 2100
tgcgtggtgg tggacgtgag ccacgaggat cccgaggtga agttcaactg gtacgtggac 2160
ggcgtggagg tgcacaatgc caagaccaag cccagagagg agcagtacaa cagcacctac 2220
agagtgggtga gcgtgctcac cgtgctgcac caggattggc tgaacggcaa ggagtacaag 2280
tgcaaggtga gcaacaaggc cctgcctgcc cccatcgaga aaaccatcag caaggccaag 2340
ggccagccca gagagcccca ggtgtacacc ctgcccccta gcagagatga gttgaccaag 2400
aaccaggtga gcctcacatg cctggtgaag ggcttctacc ccagcgacat cgccgtggag 2460
tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc 2520
gatggcagct tcttctgtga cagcaagctc accgtggaca agagcagatg gcagcagggc 2580
aacgtgttca gctgcagcgt gatgcacgag gccctgcaca atcactacac ccagaagagc 2640
ctgagcctga gccccggcaa gtaa 2664

```

<210> 26

<211> 2167

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LAMP fusion

<400> 26

```

catggagtct ccctcggccc ctccccacag atgggtgcac ccctggcaga ggctcctgct 60

```

```

cacagcctca cttctaacct tctggaaccc gccaccact gccaaagctca ctattgaatc 120
cacgccgttc aatgtcgcag aggggaagga ggtgcttcta cttgtccaca atctgcccc 180
gcatcttttt ggctacagct ggtacaaagg tgaaagagtg gatggcaacc gtcaaattat 240
aggatatgta ataggaactc aacaagctac ccagggccc gcatacagtg gtcgagagat 300
aatatacccc aatgcatccc tgctgatcca gaacatcatc cagaatgaca caggattcta 360
caccctacac gtcataaagt cagatcttgt gaatgaagaa gcaactggcc agttccgggt 420
ataccgggag ctgcccagc cctccatctc cagcaacaac tccaaaccg tggaggacaa 480
ggatgctgtg gccttcacct gtgaacctga gactcaggac gcaacctacc tgtggtgggt 540
aaacaatcag agcctcccgg tcagtcaccg gctgcagctg tccaatggca acaggacct 600
cactctattc aatgtcaca gaaatgacac agcaagctac aaatgtgaaa ccagaaccc 660
agtgagtgcc aggcgcagtg attcagtcac cctgaatgtc ctctatggcc cggatgcccc 720
caccatttcc cctctaaaca catcttacag atcaggggaa aatctgaacc tctcctgcca 780
cgcagcctct aaccacacct cacagtactc ttggtttgtc aatgggactt tccagcaatc 840
cacccaagag ctcttttatcc ccaacatcac tgtgaataat agtggatcct atacgtgcca 900
agcccataac tcagacactg gcctcaatag gaccacagtc acgacgatca cagtctatgc 960
agagccaccc aaacccttca tcaccagcaa caactccaac cccgtggagg atgaggatgc 1020
tgtagcctta acctgtgaac ctgagattca gaacacaacc tacctgtggg gggtaaataa 1080
tcagagcctc ccggtcagtc ccaggctgca gctgtccaat gacaacagga ccctcactct 1140
actcagtgtc acaaggaatg atgtaggacc ctatgagtgt ggaatccaga acgaattaag 1200
tgttgaccac agcgacccag tcatcctgaa tgcctctat ggcccagacg accccaccat 1260
ttccccctca tacacctatt accgtccagg ggtgaacctc agcctctcct gccatgcagc 1320
ctctaacca cctgcacagt attcttgggt gattgatggg aacatccagc aacacacaca 1380
agagctcttt atctccaaca tctctgagaa gaacagcgga ctctatacct gccaggccaa 1440
taactcagcc agtggccaca gcaggactac agtcaagaca atcacagtct ctgcggagct 1500
gcccagccc tccatctcca gcaacaactc caaaccctg gaggacaagg atgctgtggc 1560
cttcacctgt gaacctgagg ctgagaacac aacctacctg tgggtgggtaa atggtcagag 1620
cctcccagtc agtcccaggc tgcagctgtc caatggcaac aggacctca ctctattcaa 1680
tgtcacaaga aatgacgcaa gagcctatgt atgtggaatc cagaactcag tgagtgcaaa 1740
ccgcagtga cagtcacccc tggatgtcct ctatgggccc gacaccccca tcatttcccc 1800
cccagactcg tcttaccttt cgggagcgaa cctcaacctc tctgcccact cggcctctaa 1860
cccatccccg cagtattctt ggcgtatcaa tgggataccg cagcaacaca cacaagttct 1920
ctttatcgcc aaaatcacgc caaataataa cgggacctat gcctgttttg tctctaactt 1980
ggctactggc cgcaataatt ccatagtcaa gagcatcaca gtctctgcat ctggaactct 2040
agatgatggg aacaacatgt tgatcccat tgctgtgggc ggtgccctgg cagggtgat 2100
cctcatcgtc ctcatcgct acctcattgg caggaagagg agtcacgccg gctatcagac 2160
catctag

```

2167

<210> 27

<211> 3921

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-HSP70 fusion

<400> 27

```

atggagtctc cctcggtccc tccccacaga tgggtgcatcc cctggcagag gtcctgctc 60
acagcctcac ttctaacctt ctggaacccg cccaccactg ccaagctcac tattgaatcc 120
acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata 300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
taccgggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccctg ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccgtg cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660
gtgagtgcc aaggcagtg ttcagtcac ctgaatgtcc tctatggccc ggatgcccc 720
accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctctgccac 780
gcagcctcta acccactgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgcca 900
gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
gagccacca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtgggtg ggtaaataat 1080
cagagcctcc cggtcagtc caggctgcag ctgtccaatg acaacaggac cttcactcta 1140
ctcagtgta caaggaatga ttaggaccc tatgagtgtg gaatccagaa cgaattaagt 1200
gttgaccaca gcgaccagc catcctgaat gtcctctatg gccagacga cccaccatt 1260
tccccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg ccatgcagcc 1320
tctaaccac ctgcacagta ttcttggctg attgatggga acatccagca acacacaaa 1380
gagctcttta tctccaacat cactgagaag aacagcggac tctataacctg ccaggccaat 1440
aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgccggagctg 1500
cccaagccct ccatctccag caacaactcc aaaccctggg aggacaagga tgctgtggcc 1560
ttcacctgtg aacctgaggc tcagaacaca acctacctgt ggtgggtaaa tggtcagagc 1620
ctcccagtc gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680

```

gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gagtgcaaac 1740
 cgcagtgacc cagtcaccct ggatgtcctc tatggggcgg acacccccat catttcccc 1800
 ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggcctctaac 1860
 ccatccccgc agtattcttg gcgtatcaat gggataccgc agcaacacac acaagttctc 1920
 tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980
 gctactggcc gcaataattc catagtcaag agcatcacag tctctgcatc tggaactcta 2040
 gatatggctc gtgcggtcgg gatcgacctc gggaccacca actccgtcgt ctcggttctg 2100
 gaagggtggc acccggtcgt cgtcgccaac tccgagggct ccaggaccac cccgtcaatt 2160
 gtcgcttctc cccgcaacgg tgaggtgctg gtcggccagc ccgccaagaa ccaggcgggtg 2220
 accaacgtcg atcgaccgt gcgctcggtc aagcgacaca tgggcagcga ctggtccata 2280
 gagattgacg gcaagaaata caccgcgccg gagatcagcg cccgcattct gatgaagctg 2340
 aagcgcgacg ccgaggccta cctcgggtgag gacattaccg acgcggttat cagcagccc 2400
 gcctacttca atgacgcccc gcgtcaggcc accaaggacg ccggccagat cgcggcctc 2460
 aacgtgctgc ggatcgtcaa cgagccgacc gcggccgcgc tggcctacgg cctcgacaag 2520
 ggcgagaagg agcagcgaat cctggtcttc gacttgggtg gtggcacttt cgacgtttcc 2580
 ctgctggaga tcggcgaggg tgtggttgag gtccgtgcca cttcgggtga caaccacctc 2640
 ggcggcgacg actgggacca gcgggtcgtc gattggctgg tggacaagtt caagggcacc 2700
 agcggcatcg atctgaccaa ggacaagatg gcgatgcagc ggctgcggga agccgccgag 2760
 aaggcaaagg tcgagctgag ttcgagtcag tccacctga tcaacctgcc ctacatcacc 2820
 gtcgacgcag acaagaaccc gttgttctta gacgagcagc tgacccgcgc ggagttccaa 2880
 cggatcactc aggacctgct ggaccgcact cgcaagccgt tccagtcggt gatcgctgac 2940
 accggcattt cgggtgctgga gatcgatcac gttgtgctcg tgggtggttc gaccggatg 3000
 cccgcgggtga ccgatctggt caaggaactc accggcggca aggaacccaa caagggcgtc 3060
 aaccccgatg aggttgctgc ggtgggagcc gctctgcagg ccggcgctct caagggcgag 3120
 gtgaaagacg ttctgctgct tgatgttacc ccgctgagcc tgggtatcga gaccaagggc 3180
 ggggtgatga ccaggctcat cgagcgcaac accacgatcc cctccaagcg gtcggagact 3240
 ttcaccaccg ccgacgacaa ccaaccgtcg gtgcagatcc aggtctatca gggggagtgt 3300
 gagatcgccg cgcacaacaa gttgcccggg tccttcgagc tgaccggcat cccgccggcg 3360
 ccgcggggga ttccgcagat cgaggtcact ttcgacatcg acgccaacgg cattgtgcac 3420
 gtcaccgcca aggacaaggg caccggcaag gagaacacga tccgaatcca ggaaggctcg 3480
 ggctgtcca aggaagacat tgaccgatg atcaaggacg ccgaagcgca cgccgaggag 3540
 gatcgcaagc gtcgcgagga ggccgatgtt cgtaatcaag ccgagacatt ggtctaccag 3600
 acggagaagt tcgtcaaaga acagcgtgag gccgaggggt gttcgaaggt acctgaagac 3660
 acgtgaaca aggttgatgc cgcggtggcg gaagcgaagg cggcacttgg cggatcgat 3720
 atttcggcca tcaagtcggc gatggagaag ctgggccagg agtcgcaggc tctggggcaa 3780
 gcgatctacg aagcagctca ggctgcgtca ctggccactg gcgctgcca ccccggcggc 3840
 gagccgggcg gtgcccaccc cggctcggct gatgacgtt tggacgcgga ggtggtcgac 3900

gacggccggg aggccaagtg a

3921

<210> 28

<211> 3585

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-VSVG fusion

<400> 28

```

atggagtctc cctcggtccc tccccacaga tgggtgcatcc cctggcagag gtccttgctc 60
acagcctcac ttctaacctt ctggaacccg cccaccactg ccaagctcac tattgaatcc 120
acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata 300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
tacccgagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480
gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccgtt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660
gtgagtgccg ggcgcagtga ttcagtcac ctgaatgtcc tctatggccc ggatgcccc 720
accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctctgtccac 780
gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgcca 900
gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
gagccacca aaccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg ggtaaataat 1080
cagagcctcc cggtcagtcc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140
ctcagtgtca caaggaatga ttaggaccc tatgagtgtg gaatccagaa cgaattaagt 1200
gttgaccaca gcgaccagc catcctgaat gtcctctatg gccagacga cccaccatt 1260
tccccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg ccatgcagcc 1320
tctaaccac ctgcacagta ttcttggtg attgatggga acatccagca acacacaaa 1380
gagctcttta tctccaacat cactgagaag aacagcggac tctataacct ccaggccaat 1440
aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgccgagctg 1500
cccaagccct ccatctccag caacaactcc aaaccctggg aggacaagga tgctgtggcc 1560

```

```

ttcacctgtg aacctgaggc tcagaacaca acctacctgt ggtgggtaaa tggtcagagc 1620
ctcccagtcg gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680
gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gaggcgaaac 1740
cgcagtgacc cagtcaccct ggatgtcctc tatggggccg acacccccat catttcccc 1800
ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggctctaac 1860
ccatccccgc agtattcttg gcgtatcaat gggataccgc agcaacacac acaagttctc 1920
tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980
gctactggcc gcaataattc catagtcaag agcatcacag tctctgcatc tggaactcta 2040
gatgaattca tgaagtgctt tttgtactta gcttttttat tcatcggggg gaattgcaag 2100
ttcaccatag tttttccaca caaccaaaaa ggaaactgga aaaatgttcc ttccaattac 2160
cattattgcc cgtcaagctc agattttaat tggcataatg acttaatagg cacaggctta 2220
caagtcaaaa tgcccaagag tcacaaggct attcaagcag acggttgat gtgtcatgct 2280
tccaaatggg tcaactcttg tgatttccgc tggtagcgac cgaagtatat aacacattcc 2340
atccgatcct tcactccatc tgtagaacaa tgcaaggaaa gcattgaaca aacgaaacaa 2400
ggaacttggc tgaatccagg cttccctcct caaagttgtg gatatgcaac tgtgacggat 2460
gccgaagcag tgattgtcca ggtgactcct caccatgtgc ttgttgatga atacacagga 2520
gaatggggtt attcacagtt catcaacgga aaatgcagca atgacatatg cccactgtc 2580
cataactcca caacctggca ttccgactat aagggtcaaag ggctatgtga ttctaacctc 2640
atttccacgg acatcacctt cttctcagag gacagagagc tatcatccct aggaaaggag 2700
ggcacagggt tcagaagtaa ctactttgct tatgaaactg gagacaaggc ctgcaaaatg 2760
cagtactgca agcattgggg agtcagactc ccacaggtg tctgggtcga gatggctgat 2820
aaggatctct ttgctgcagc cagattccct gaatgccag aagggtcaag tatctctgct 2880
ccatctcaga cctcagtgga tgtaagtctc attcaggacg ttgagaggat cttggattat 2940
tcctctgcc aagaaacctg gagcaaaatc agagcgggtc tcccatctc tccagtggat 3000
ctcagctatc ttgctcctaa aaaccagga accggtcctg cctttaccat aatcaatggt 3060
accctaaaat actttgagac cagatacatc agagtcgata ttgctgctcc aatcctctca 3120
agaatggctg gaatgatcag tggaaactacc acagaaaggg aactgtggga tgactgggct 3180
ccatatgaag acgtggaaat tggacccaat ggagttctga ggaccagttc aggatataag 3240
tttcttttat atatgattgg acatggtatg ttggactccg gtcttcatct tagctcaaag 3300
gctcaggtgt ttgaacatcc tcacattcaa gacgtgctt cgcagcttcc tgatgatgag 3360
attttatttt ttggtgatac tgggctatcc aaaaatccaa tcgactttgt cgaaggttgg 3420
ttcagtagtt ggaagagctc cattgcctct tttttcttta tcatagggtt aatcattgga 3480
ctattcttgg ttctccgagt tggattttat ctttacatta aattaaagca caccaagaaa 3540
agacagattt atacagacat agagatgaac cgacttgga ggtaa 3585

```

<210> 29

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 29

tattctagat tcaacaccaa ttccattttc ttattc

36

<210> 30

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 30

gcggcgcgcta gaatcatttg tccatccttc atc

33

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 31

tattctagat tcaacaccaa ttccattttc ttattc

36

<210> 32

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 32

ttagcgggcg ctagttctgt atcatatcgt aaaggg

36

<210> 33

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 33

tctagataaa actcacacat gccca

25

<210> 34

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 34

gccgactcat ttacccggag acagggag

28

<210> 35

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 35

tctagatttg atccccattg ctgtgggcgg tgccctg

37

<210> 36

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 36

ggcgtgactc ctcttcctgc caatgaggta ggcaatgag

39

<210> 37

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 37

atatctagat ttcacccatag tttttccaca caacc

35

<210> 38

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 38

gcggcgcct tccttccaag tcggttcac tctatg

36

<210> 39

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 39

gctctagata tggctcgtgc ggtcgggatc gacc

34

<210> 40

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 40

gccgcggccg ctcaacttggc ctcccggccg tcgtcg

36

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 41

gttatctaga agcaccceca tccc

24

<210> 42

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer, chemically synthesized

<400> 42
ttaagatctc taagatctgg tgcgtatct cagggg 36

<210> 43
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer, chemically synthesized

<400> 43
ttatctagaa agaccacac ctgccccct tgc 33

<210> 44
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer, chemically synthesized

<400> 44
tatagatctt agggtacctt acttgccggg g 31

<210> 45
<211> 952
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA-Dom fusion

<400> 45
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15

Arg	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr			
			20						25					30				
Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly			
		35						40				45						
Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly			
		50				55					60							
Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile			
65					70					75					80			
Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser			
			85						90					95				
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile			
			100					105					110					
Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp			
		115					120					125						
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu			
		130				135					140							
Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys			
145					150					155					160			
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr			
			165						170				175					
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln			
			180					185					190					
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn			
		195					200					205						
Asp	Thr	Ala	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Ala	Arg			
		210				215					220							
Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro			
225					230					235					240			
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn			
			245						250					255				
Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	Trp	Phe			
			260					265					270					
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn			
		275					280					285						
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala	His	Asn	Ser			
		290				295					300							
Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr	Val	Tyr	Ala			

305	310	315	320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu			
325	330	335	
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr			
340	345	350	
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg			
355	360	365	
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr			
370	375	380	
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser			
385	390	395	400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp			
405	410	415	
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn			
420	425	430	
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser			
435	440	445	
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile			
450	455	460	
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn			
465	470	475	480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val			
485	490	495	
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro			
500	505	510	
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln			
515	520	525	
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser			
530	535	540	
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn			
545	550	555	560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser			
565	570	575	
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly			
580	585	590	
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly			
595	600	605	

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln			
610	615	620	
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu			
625	630	635	640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe			
645	650	655	
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile			
660	665	670	
Thr Val Ser Ala Ser Gly Thr Ser Arg Ser Thr Pro Ile Pro Phe Ser			
675	680	685	
Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp			
690	695	700	
Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp			
705	710	715	720
Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro			
725	730	735	
Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val			
740	745	750	
Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu			
755	760	765	
Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val			
770	775	780	
Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr			
785	790	795	800
Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly			
805	810	815	
Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp			
820	825	830	
Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys			
835	840	845	
Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn			
850	855	860	
Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly			
865	870	875	880
Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile			
885	890	895	
Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile			

900	905	910
Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu		
915	920	925
Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp		
930	935	940
Gly Asn Pro Leu Arg Tyr Asp Thr		
945	950	

<210> 46

<211> 907

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-FcIgG fusion

<400> 46

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln		
1	5	10
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr		
20	25	30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly		
35	40	45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly		
50	55	60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile		
65	70	75
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser		
85	90	95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile		
100	105	110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp		
115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys		

145	150	155	160												
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr
	165		170		175										
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln
	180		185		190										
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn
	195		200		205										
Asp	Thr	Ala	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Ala	Arg
	210		215		220										
Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro
225			230		235										240
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn
	245		250		255										
Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	Trp	Phe
	260		265		270										
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn
	275		280		285										
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala	His	Asn	Ser
	290		295		300										
Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr	Val	Tyr	Ala
305			310		315										320
Glu	Pro	Pro	Lys	Pro	Phe	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu
	325		330		335										
Asp	Glu	Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Ile	Gln	Asn	Thr
	340		345		350										
Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg
	355		360		365										
Leu	Gln	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Leu	Leu	Ser	Val	Thr
	370		375		380										
Arg	Asn	Asp	Val	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Glu	Leu	Ser
385			390		395										400
Val	Asp	His	Ser	Asp	Pro	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp
	405		410		415										
Asp	Pro	Thr	Ile	Ser	Pro	Ser	Tyr	Thr	Tyr	Tyr	Arg	Pro	Gly	Val	Asn
	420		425		430										
Leu	Ser	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser
	435		440		445										


```

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
  450                      455                      460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465                      470                      475                      480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
                      485                      490                      495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
                      500                      505                      510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
                      515                      520                      525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
                      530                      535                      540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545                      550                      555                      560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
                      565                      570                      575
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
                      580                      585                      590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
                      595                      600                      605
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
                      610                      615                      620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625                      630                      635                      640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
                      645                      650                      655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
                      660                      665                      670
Thr Val Ser Ala Ser Gly Thr Ser Arg Lys Thr His Thr Cys Pro Pro
                      675                      680                      685
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
                      690                      695                      700
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
705                      710                      715                      720
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
                      725                      730                      735
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

```

740	745	750
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val		
755	760	765
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser		
770	775	780
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys		
785	790	795
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp		
805	810	815
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe		
820	825	830
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu		
835	840	845
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe		
850	855	860
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly		
865	870	875
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr		
885	890	895
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
900	905	

<210> 47

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<223> N-terminal domain of fragment C of tetanus toxin

<400> 47

gattcaacac caattccatt ttcttattct aaaaatctgg attggtgggt tgataatgaa 60
gaagatatag atgttatatt aaaaaagagt acaattttta attagatat taataatgat 120
attatatcag atatatctgg gtttaattca tctgtaataa catatccaga tgctcaattg 180
gtgcccggaa taaatggcaa agcaatacat ttagtaaaca atgaatcttc tgaagttata 240
gtgcataaag ctatggatat tgaatataat gatatgttta ataattttac cgtagcttt 300

```

tggttgaggg ttcctaaagt atctgctagt catttagaac aatatggcac aaatgagtat 360
tcaataatta gctctatgaa aaaacatagt ctatcaatag gatctgggtg gagtgtatca 420
cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 480
acttttaggg atttacctga taaatttaat gcttatttag caaataaatg ggtttttata 540
actattacta atgatagatt atcttctgct aatttgata taaatggagt acttatggga 600
agtgcagaaa ttactgggtt aggagctatt agagaggata ataataaac attaaaacta 660
gatagatgta ataataataa tcaatacgtt tctattgata aatttaggat attttgcaaa 720
gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aaccttttta 780
agagacttct ggggaaaccc tttagcatat gatacagata ggtag                               825

```

<210> 48

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> N-terminal domain of fragment C of tetanus toxin

<400> 48

```

Asp Ser Thr Pro Ile Pro Phe Ser Tyr Ser Lys Asn Leu Asp Cys Trp
 1             5             10             15
Val Asp Asn Glu Glu Asp Ile Asp Val Ile Leu Lys Lys Ser Thr Ile
          20             25             30
Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser Gly Phe
          35             40             45
Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro Gly Ile
          50             55             60
Asn Gly Lys Ala Ile His Leu Val Asn Asn Glu Ser Ser Glu Val Ile
65             70             75             80
Val His Lys Ala Met Asp Ile Glu Tyr Asn Asp Met Phe Asn Asn Phe
          85             90             95
Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu
          100            105            110
Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met Lys Lys
          115            120            125
His Ser Leu Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys Gly Asn
          130            135            140

```

Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg Gln Ile
 145 150 155 160
 Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys
 165 170 175
 Trp Val Phe Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu
 180 185 190
 Tyr Ile Asn Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly Leu Gly
 195 200 205
 Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn
 210 215 220
 Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys
 225 230 235 240
 Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser
 245 250 255
 Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
 260 265 270
 Asp Arg

<210> 49

<211> 2857

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-DOM fusion

<400> 49

atggagtctc cctcggtccc tccccacaga tgggtgcatcc cctggcagag gctcctgctc 60
 acagcctcac ttctaacctt ctggaaccg cccaccactg ccaagctcac tattgaatcc 120
 acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
 catcttttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
 ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata 300
 atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
 accctacacg tcataaagtc agatcttggtg aatgaagaag caactggcca gttccgggta 420
 taccgggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480

gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta 540
aacaatcaga gcctcccggg cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660
gtgagtgcc a ggcgcagtga ttcagtcac cctgaatgtcc tctatggccc ggatgcccc 720
accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctctgccac 780
gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgccaa 900
gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgca 960
gagccacca aacccttcat caccagcaac aactccaacc ccgtggagga tgaggatgct 1020
gtagccttaa cctgtgaacc tgagattcag aacacaacct acctgtggtg ggtaaataat 1080
cagagcctcc cggtcagtc caggctgcag ctgtccaatg acaacaggac cctcactcta 1140
ctcagtgta caaggaatga ttaggaccc tatgagtgtg gaatccagaa cgaattaagt 1200
gttgaccaca gcgacccagt catcctgaat gtcctctatg gccagacga cccaccatt 1260
tccccctcat acacctatta ccgtccaggg gtgaacctca gcctctcctg catgacgac 1320
tctaaccac ctgcacagta ttcttggtg attgatggga acatccagca acacacaaa 1380
gagctcttta tctccaacat cactgagaag aacagcggac tctataacctg ccaggccaat 1440
aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgccggagctg 1500
cccaagccct ccatctccag caacaactcc aaaccctgg aggacaagga tgctgtggcc 1560
ttcacctgtg aacctgaggg tcagaacaca acctacctgt ggtgggtaaa tggtcagagc 1620
ctcccagtc gtcccaggct gcagctgtcc aatggcaaca ggaccctcac tctattcaat 1680
gtcacaagaa atgacgcaag agcctatgta tgtggaatcc agaactcagt gagtgcacaa 1740
cgcagtgacc cagtcacct ggatgtctc tatgggcccg acacccccat catttcccc 1800
ccagactcgt cttacctttc gggagcgaac ctcaacctct cctgccactc ggctctaac 1860
ccatccccgc agtattcttg gcgtatcaat gggataccgc agcaacacac acaagtctc 1920
tttatcgcca aaatcacgcc aaataataac gggacctatg cctgttttgt ctctaacttg 1980
gctactggcc gcaataattc catagtcaag agcatcacag tctctgcac tggaactcta 2040
gattcaacac caattccatt ttcttattct aaaaatctgg attgttgggt tgataatgaa 2100
gaagatatag atgttatatt aaaaaagagt acaattttta atttagatat taataatgat 2160
attatatcag atatatctgg gtttaattca tctgtaataa catatccaga tgctcaattg 2220
gtgcccggaa taaatggcaa agcaatacat ttagtaacaa atgaatcttc tgaagttata 2280
gtgcataaag ctatggatat tgaatataat gatatgttta ataattttac cgttagcttt 2340
tggttgaggg ttcctaaagt atctgctagt catttagaac aatatggcac aatgagtat 2400
tcaataatta gctctatgaa aaaacatagt ctatcaatag gatctgggtg gagtgtatca 2460
cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 2520
acttttaggg atttacctga taaatttaat gcttatttag caaataaatg ggtttttata 2580
actattacta atgatagatt atcttctgct aatttgata taaatggagt acttatggga 2640
agtgcagaaa ttactgggtt aggagctatt agagaggata ataataaac attaaaacta 2700

gatagatgta ataataataa tcaatacgtt tctattgata aatttaggat attttgcaaa 2760
gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aaccttttta 2820
agagacttct ggggaaaccc ttacgatat gatatag 2857

<210> 50

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 50

atgggcagcc ccagcgcccc cctgcaccgc tgggtgcatcc cctggcagac cctgctgctg 60
accgccagcc tgctgacctt ctggaacccc cccaccaccg cccagctgac catcgagagc 120
cgcccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
agctgctgta tccgcaccca gcagatcacc cccggccccg cccacagcgg ccgcgagacc 300
atcgacttca acgccagcct gctgatccac aacgtgaccc agagcgacac cggcagctac 360
accatccagg tgatcaagga ggacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccgccagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccggt ggaggacaag 480
gacgccgtgg ccctgacctg cgagcccagc acccaggaca ccacctacct gtggtggggtg 540
aacaaccaga gcctgcccgt gagcccccg cctggagctga gcagcgacaa ccgcaccctg 600
accgtgttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
gtgagcgtgc gccgcagcga ccccgtagcc ctgaacgtgc tgtacggccc cgacgcccc 720
accatcagcc ccctgaacac cccctaccgc gccggcgaga acctgaacct gacctgccac 780
gccgccagca accccaccgc ccagtacttc tggttcgtga acggcacctt ccagcagagc 840
accaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta catgtgccag 900
gccacaaca gcgccaccgg cctgaaccgc accaccgtga ccgccatcac cgtgtacgcc 960
gagctgccc aagccctacat caccagcaac aacagcaacc ccatcgagga caaggacgcc 1020
gtgaccctga cctgcgagcc cgagaccagc gacaccacct acctgtggtg ggtgaacaac 1080
cagagcctga gcgtgagcag ccgcctggag ctgagcaacg acaaccgcac cctgaccgtg 1140
ttcaacatcc cccgcaacga caccaccttc tacgagtgcg agaccagaa ccccgtagc 1200
gtgcgccga gcgaccccg gacctgaac gtgctgtacg gccccgacgc cccaccatc 1260
agccccctga acacccccta ccgcgccggc gagaacctga acctgagctg ccacgccgcc 1320
agcaaccccg ccgccagta cagctgggtc gtgaacggca ccttcagca gagcaccag 1380
gagctgttca tccccaat caccgtgaac aacagcggca gctacatgtg ccaggccac 1440

```

aacagcgcca ccggcctgaa ccgcaccacc gtgaccgcca tcaccgtgta cgtggagctg 1500
cccaagccct acatcagcag caacaacagc aaccccatcg aggacaagga cgccgtgacc 1560
ctgacctgcg agcccgtggc cgagaacacc acctacctgt ggtgggtgaa caaccagagc 1620
ctgagcgtga gccccgcct gcagctgagc aacggcaacc gcatcctgac cctgctgagc 1680
gtgaccgca acgacaccgg ccctacgag tgcggcatcc agaacagcga gagcgccaag 1740
cgcagcgacc ccgtgaccct gaacgtgacc tacggccccg acaccccat catcagcccc 1800
cccgacctga gctaccgag cggcgccaac ctgaacctga gctgccacag cgacagcaac 1860
cccagcccc agtacagctg gctgatcaac ggcaccctgc gccagcacac ccaggtgctg 1920
ttcatcagca agatcaccag caacaacagc ggcgcctacg cctgcttcgt gagcaacctg 1980
gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040
agaagcacc ccattccatt cagctacagc aagaacctgg actgctgggt ggacaacgag 2100
gaggacatcg acgtgatcct gaagaagagc accatcctga acctggacat caacaacgac 2160
atcatcagcg acatcagcgg cttcaacagc agcgtgatca cctacccga cgcccagctg 2220
gtgcccggca tcaacggcaa ggccatccac ctggtgaaca acgagagcag cgaggtgatc 2280
gtgcacaagg ccatggacat cgagtacaac gacatgttca acaacttcac cgtgagcttc 2340
tggtgagag tgcctaaggt gagcgccagc cacctggagc agtacggcac caacgagtac 2400
agcatcatca gcagcatgaa gaagcacagc ctgagcatcg gcagcggctg gagcgtgagc 2460
ctgaagggca acaacctcat ctggaccctg aaggatagcg ccggagaggt gagacagatc 2520
accttcagag acctgcccga caagttcaat gcctacctgg ccaacaagtg ggtgttcac 2580
accatcacca acgacagact gagcagcgcc aacctgtaca tcaacggcgt gctcatgggc 2640
agcgccgaga tcaccggcct gggcgccatc agagaggaca acaacatcac cctgaagctg 2700
gacagatgca acaacaacaa ccagtacgtg agcatcgaca agttccggat cttctgcaag 2760
gccctgaacc ccaaggagat cgagaagctg tacaccagct acctgagcat caccttcctg 2820
agagacttct ggggcaaccc cctgagatac gacacctag 2859

```

<210> 51

<211> 952

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 51

Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln

1

5

10

15

Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr

20	25	30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly		
35	40	45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly		
50	55	60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly		
65	70	75
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser		
85	90	95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val		
100	105	110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp		
115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys		
145	150	155
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr		
165	170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu		
180	185	190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn		
195	200	205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg		
210	215	220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn		
245	250	255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser		
290	295	300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala		
305	310	315
		320

Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Ile	Glu			
				325					330					335				
Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr			
			340					345					350					
Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser	Ser	Arg			
		355				360						365						
Leu	Glu	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro			
	370					375					380							
Arg	Asn	Asp	Thr	Thr	Phe	Tyr	Glu	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser			
385					390					395				400				
Val	Arg	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp			
			405					410				415						
Ala	Pro	Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn			
		420					425					430						
Leu	Asn	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Ala	Ala	Gln	Tyr	Ser			
	435					440						445						
Trp	Phe	Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile			
	450					455					460							
Pro	Asn	Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Met	Cys	Gln	Ala	His			
465				470						475				480				
Asn	Ser	Ala	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Ala	Ile	Thr	Val			
			485					490				495						
Tyr	Val	Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro			
		500					505					510						
Ile	Glu	Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Val	Ala	Glu			
	515						520					525						
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser			
	530					535					540							
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Ile	Leu	Thr	Leu	Leu	Ser			
545				550						555				560				
Val	Thr	Arg	Asn	Asp	Thr	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Ser			
			565					570				575						
Glu	Ser	Ala	Lys	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Thr	Tyr	Gly			
		580						585				590						
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Leu	Ser	Tyr	Arg	Ser	Gly			
	595					600						605						
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Asp	Ser	Asn	Pro	Ser	Pro	Gln			

610	615	620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu		
625	630	635
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe		640
645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile		
660	665	670
Ser Val Ser Ser Gly Asp Ser Ser Arg Ser Thr Pro Ile Pro Phe Ser		
675	680	685
Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp		
690	695	700
Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp		
705	710	715
Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro		720
725	730	735
Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val		
740	745	750
Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu		
755	760	765
Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val		
770	775	780
Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr		
785	790	795
Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly		800
805	810	815
Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp		
820	825	830
Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys		
835	840	845
Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn		
850	855	860
Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly		
865	870	875
Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile		880
885	890	895
Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile		
900	905	910

Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu
 915 920 925
 Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp
 930 935 940
 Gly Asn Pro Leu Arg Tyr Asp Thr
 945 950

<210> 52

<211> 2359

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-CTBopt fusion

<400> 52

atgggcagcc ccagcgcccc cctgcaccgc tgggtgcatcc cctggcagac cctgctgctg 60
 accgccagcc tgctgacctt ctggaacccc cccaccaccg cccagctgac catcgagagc 120
 cgcccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
 aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
 agctgctgta tccgcaccca gcagatcacc cccggccccg cccacagcgg ccgcgagacc 300
 atcgacttca acgccagcct gctgatccac aacgtgaccc agagcgacac cggcagctac 360
 accatccagg tgatcaagga ggacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
 taccgccagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccggt ggaggacaag 480
 gacgccgtgg ccctgacctg cgagcccagc acccaggaca ccacctacct gtggtgggtg 540
 aacaaccaga gcctgcccgt gagcccccg cctggagctga gcagcgacaa ccgcaccctg 600
 accgtgttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
 gtgagcgtgc gccgcagcga ccccgtagacc ctgaacgtgc tgtacggccc cgacgcccc 720
 accatcagcc ccctgaacac cccctaccgc gccggcgaga acctgaacct gacctgccac 780
 gccgccagca accccaccgc ccagtacttc tggttcgtga acggcacctt ccagcagagc 840
 acccaggagc tgttcatccc caacatcacc gtgaacaaca gcggcagcta catgtgccag 900
 gccacaaca gcgccaccgg cctgaaccgc accaccgtga ccgccatcac cgtgtacgcc 960
 gagtgccca agccctacat caccagcaac aacagcaacc ccatcgagga caaggacgcc 1020
 gtgaccctga cctgcgagcc cgagaccagc gacaccacct acctgtggtg ggtgaacaac 1080
 cagagcctga gcgtgagcag ccgcctggag ctgagcaacg acaaccgcac cctgaccgtg 1140
 ttcaacatcc cccgcaacga caccaccttc tacgagtgcg agaccagaa ccccgtagc 1200

```

gtgcgccgca gcgaccccggt gaccctgaac gtgctgtacg gccccgacgc cccaccatc 1260
agccccctga acacccccta ccgcgccggc gagaacctga acctgagctg ccacgccgcc 1320
agcaaccccg ccgcccagta cagctggttc gtgaacggca ccttcagca gagcacccag 1380
gagctgttca tccccaacat caccgtgaac aacagcggca gctacatgtg ccaggccac 1440
aacagcgcca ccggcctgaa ccgcaccacc gtgaccgcca tcaccgtgta cgtggagctg 1500
cccaagccct acatcagcag caacaacagc aaccccatcg aggacaagga cgccgtgacc 1560
ctgacctgcg agcccgaggc cgagaacacc acctacctgt ggtgggtgaa caaccagagc 1620
ctgagcgtga gccccgcct gcagctgagc aacggcaacc gcatcctgac cctgctgagc 1680
gtgacccgca acgacaccgg cccctacgag tgcggcatcc agaacagcga gagcgccaag 1740
cgcagcgacc ccgtgaccct gaacgtgacc tacggccccg acacccccat catcagcccc 1800
cccgacctga gctaccgcag cggcgccaac ctgaacctga gctgccacag cgacagcaac 1860
cccagcccc agtacagctg gctgatcaac ggcaccctgc gccagcacac ccaggtgctg 1920
ttcatcagca agatcaccag caacaacagc ggcgcctacg cctgcttcgt gagcaacctg 1980
gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040
agaaccctc agaacatcac cgatctgtgc gccgagtacc acaacacca gatctacacc 2100
ctgaacgaca agatcttcag ctacaccgag agcctggccg gcaagagaga gatggccatc 2160
atcaccttca agaacggcgc catcttcag gtggaggtgc ccggcagcca gcacatcgac 2220
agccagaaga aggccatcga gcggatgaag gacaccctgc ggatcgcta cctcaccgag 2280
gccaaggtgg agaagctgtg cgtgtggaac aacaagacc ctcacgcat cgccgccatc 2340
agcatggcca attgataag 2359

```

<210> 53

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-CTBopt fusion

<400> 53

```

Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
  1             5             10             15
Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
      20             25             30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
      35             40             45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly

```

50	55	60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly		
65	70	75
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser		80
85	90	95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val		
100	105	110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp		
115	120	125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu		
130	135	140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys		
145	150	155
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr		160
165	170	175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu		
180	185	190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn		
195	200	205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg		
210	215	220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro		
225	230	235
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn		240
245	250	255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe		
260	265	270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn		
275	280	285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser		
290	295	300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala		
305	310	315
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu		320
325	330	335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr		
340	345	350

```

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
      355                      360                      365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
      370                      375                      380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
385                      390                      395                      400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
      405                      410                      415
Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
      420                      425                      430
Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
      435                      440                      445
Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
      450                      455                      460
Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
465                      470                      475                      480
Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
      485                      490                      495
Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
      500                      505                      510
Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
      515                      520                      525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
      530                      535                      540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
545                      550                      555                      560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
      565                      570                      575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
      580                      585                      590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
      595                      600                      605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
      610                      615                      620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
625                      630                      635                      640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe

```

	645		650		655										
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Asn	Ile
	660		665		670										
Ser	Val	Ser	Ser	Gly	Asp	Ser	Ser	Arg	Thr	Pro	Gln	Asn	Ile	Thr	Asp
	675		680		685										
Leu	Cys	Ala	Glu	Tyr	His	Asn	Thr	Gln	Ile	Tyr	Thr	Leu	Asn	Asp	Lys
	690		695		700										
Ile	Phe	Ser	Tyr	Thr	Glu	Ser	Leu	Ala	Gly	Lys	Arg	Glu	Met	Ala	Ile
705			710		715										720
Ile	Thr	Phe	Lys	Asn	Gly	Ala	Ile	Phe	Gln	Val	Glu	Val	Pro	Gly	Ser
	725		730		735										
Gln	His	Ile	Asp	Ser	Gln	Lys	Lys	Ala	Ile	Glu	Arg	Met	Lys	Asp	Thr
	740		745		750										
Leu	Arg	Ile	Ala	Tyr	Leu	Thr	Glu	Ala	Lys	Val	Glu	Lys	Leu	Cys	Val
	755		760		765										
Trp	Asn	Asn	Lys	Thr	Pro	His	Ala	Ile	Ala	Ala	Ile	Ser	Met	Ala	Asn
	770		775		780										

<210> 54

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> chemically synthesized

<400> 54

Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala

1

5

10

15

Ser His Leu Glu

20